

JAGuaR Alignment

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 An abbreviated version of this protocol was published in Frontiers in Genetics in Jun 2021
A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells
DOI: 10.3389/fgene.2021.665888

Detailed protocol

The **JAGuaR** analysis pipeline was initially described in <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0102398>.

Briefly, short reads are aligned with BWA mem against a reference containing known exon-exon junctions and the hg19 genome. After alignment, reads aligning to the exon-exon junctions are placed back into the canonical reference genome at a location surrounding the detected splice site.

Instructions to perform this analysis are available at this location:
<https://svn.bcgsc.ca/bitbucket/projects/RCORBETT/repos/jaguar/browse>

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Corbett, R. (2022). JAGuaR Alignment. Bio-protocol Preprint. bio-protocol.org/prep1643.
2. Haile, S., Corbett, R. D., LeBlanc, V. G., Wei, L., Pleasance, S., Bilobram, S., Nip, K. M., Brown, K., Trinh, E., Smith, J., Trinh, D. L., Bala, M., Chuah, E., Coope, R. J. N., Moore, R. A., Mungall, A. J., Mungall, K. L., Zhao, Y., Hirst, M., Aparicio, S., Birol, I., Jones, S. J. M. and Marra, M. A. (2021). A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. Frontiers in Genetics 0(0). DOI: [10.3389/fgene.2021.665888](https://doi.org/10.3389/fgene.2021.665888)

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